

***Amendments to the Specification***

***In the Drawings***

Please delete Figures 29A, 29B, and 29C.

Please substitute Figures 3, 13, 14, 15, 30, and 31 with the attached Figures 3, 13,  
14, 15, 29A, 29B, and 30.

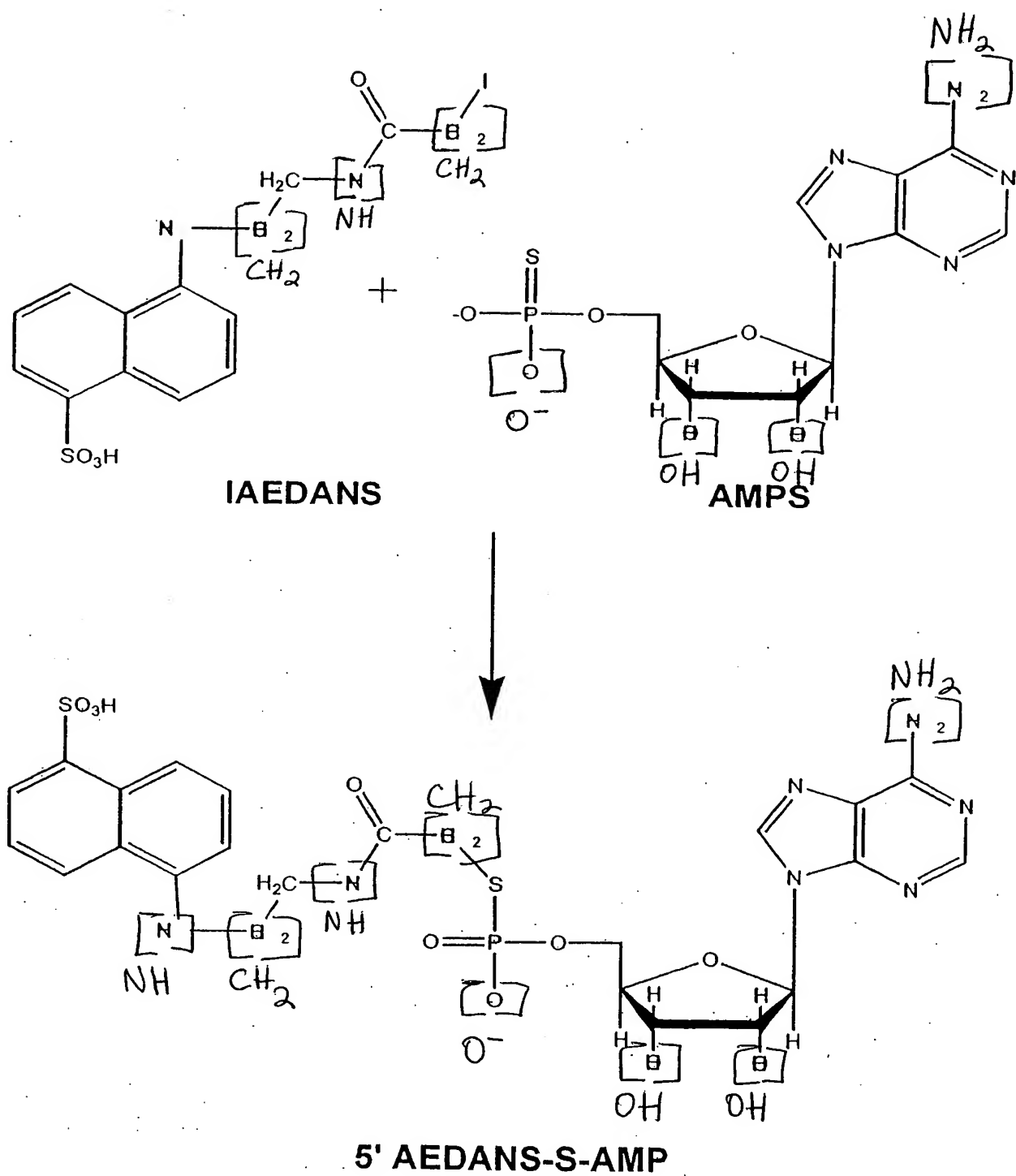


FIGURE 3

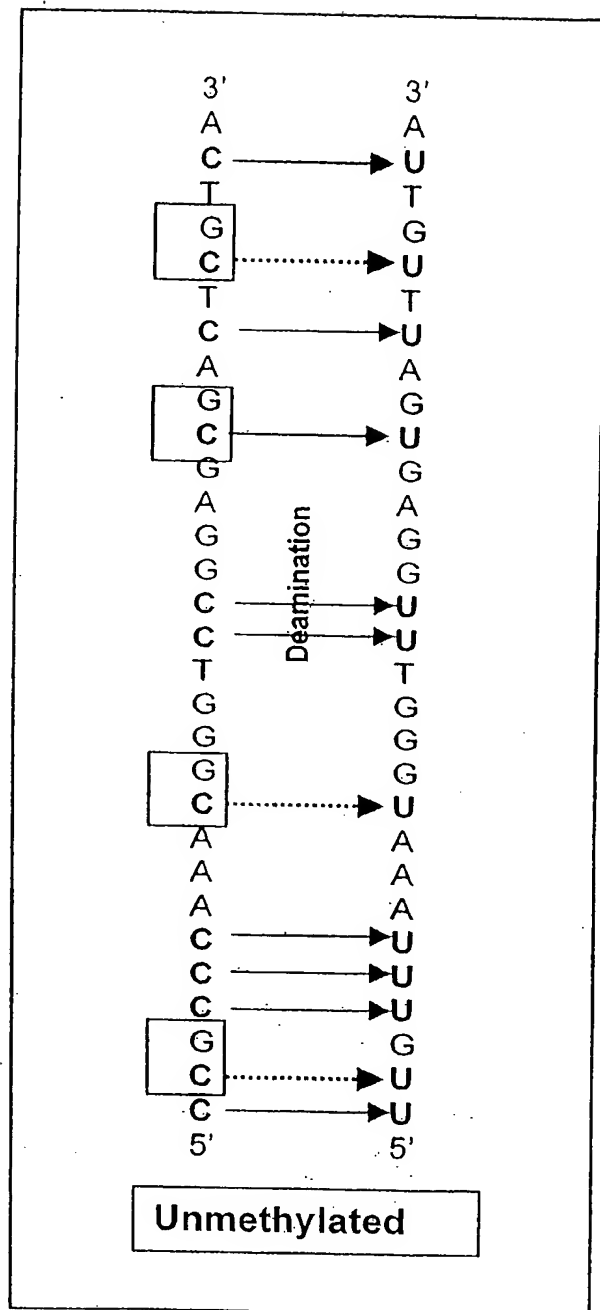
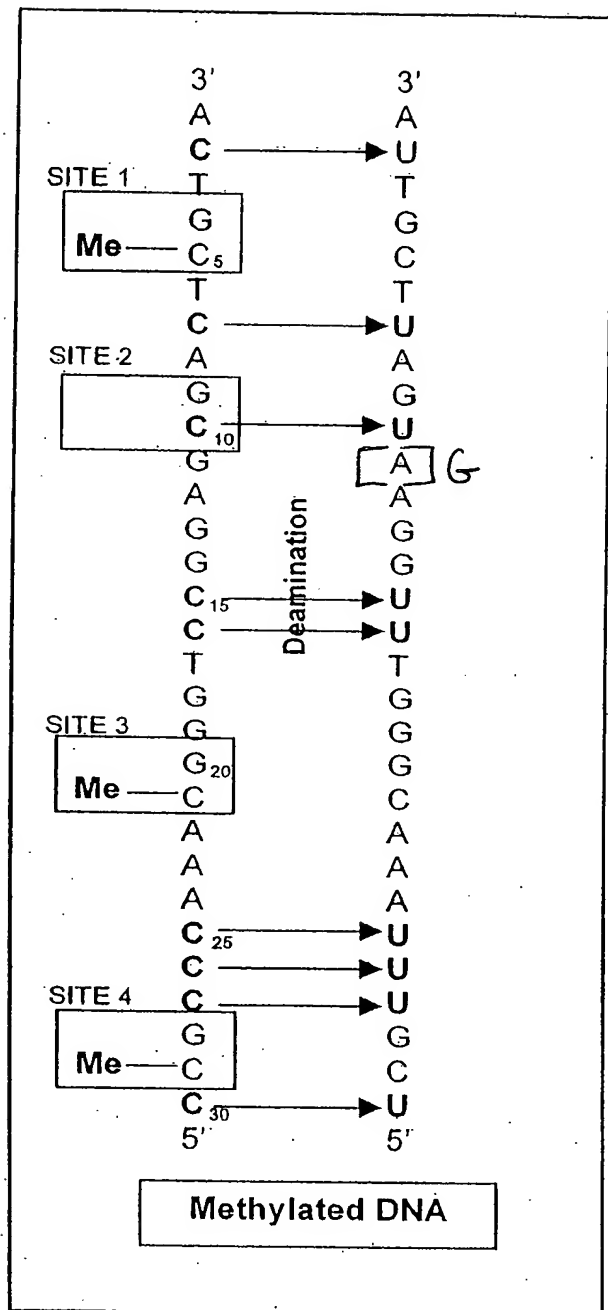


FIGURE 13

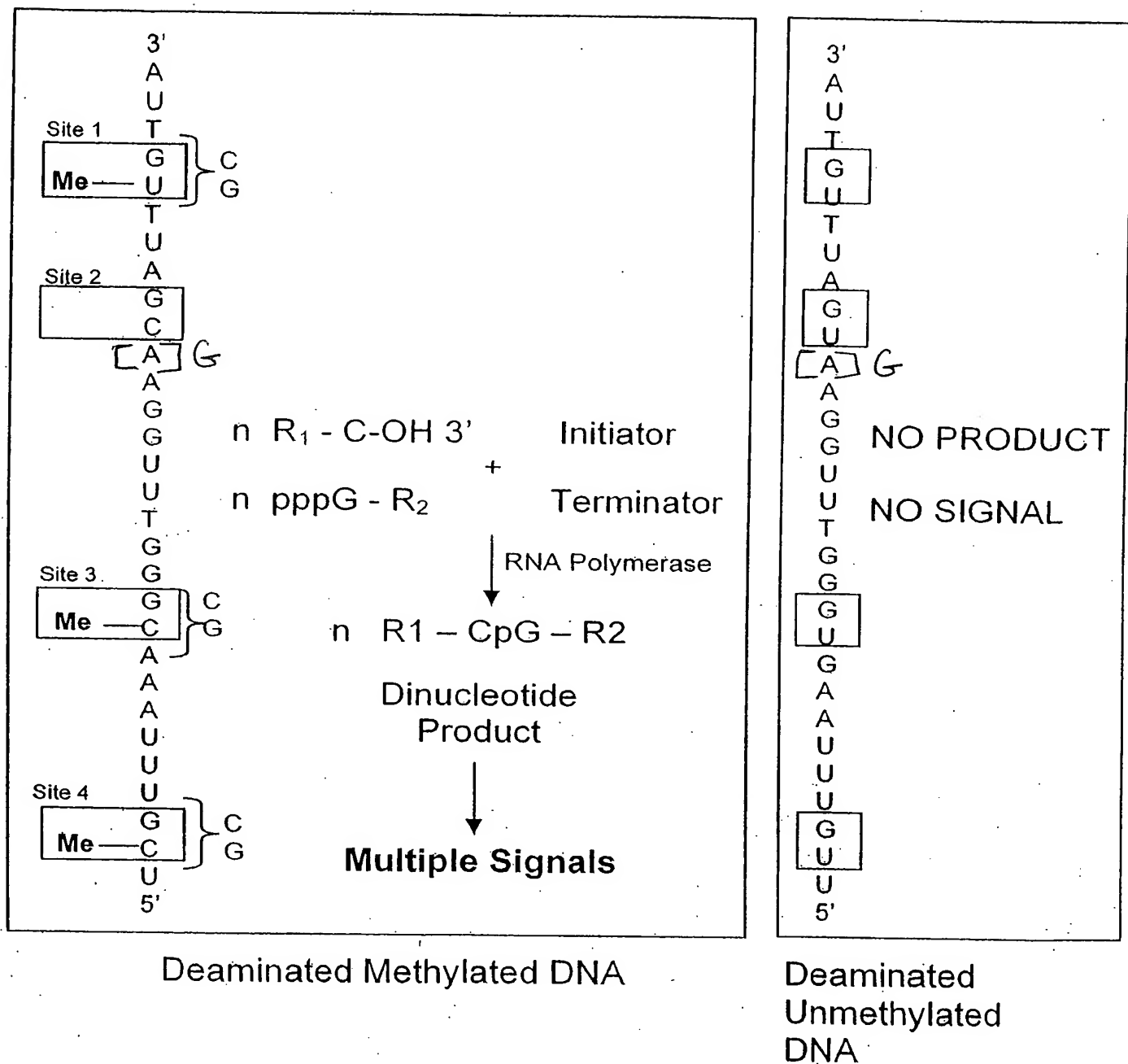
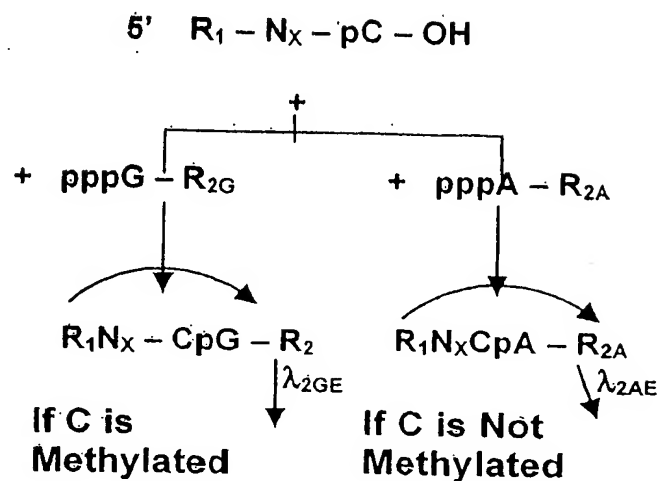
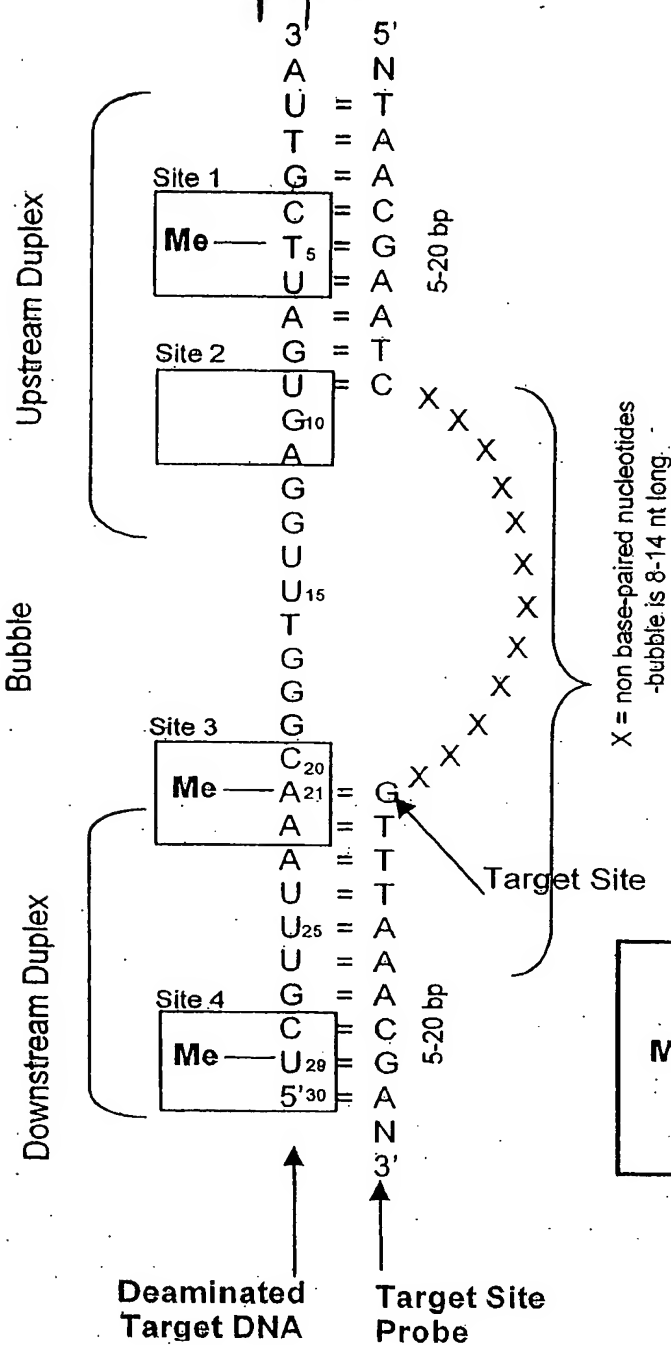


FIGURE 14

entire nucleotide strand  
moved down by 1 nucleotide  
so that bases pair correctly



- $M = 1$  If both copies are 100% methylated: Only  $\lambda_{2GE}$  detected
- $M = 0.5$  If 1 copy is methylated: Both  $\lambda_{2GE}$  and  $\lambda_{2AE}$  detected
- $M = 0$  If both copies unmethylated: only  $\lambda_{2AE}$  detected

$$M = \text{Methylation Index} = \frac{E\lambda_{2GE}}{E\lambda_{2GE} + E\lambda_{2GA}}$$

FIGURE 15

ATTATCCAGT  
 AGGCAGATTAAGCATGTGCTTAAGGCATCAGCAAAGTCTGAGCAATCCATTTTTTAAAACGTAGTACATGTTTT  
 TGATAAGCTTAAAAAGTAGTAGTCACAGGAAAAATTAGAACTTTTACCTCCTTGCGCTTGTTATACTCTTTAGT  
 GCTGTTTAACTTTTCTTTGTAAGTGAGGGTGGTGGAGGGTGCCCATAACTCTTTTCAGGGAGTAAGTTCTTCTT  
 GGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTGAGACCAAGTTTCGCTCTTGTCTCCAGGCTGGAGTGCAA  
 TGGCGCGATCTCGGCTCACTGCAACCTCCGCCTTCTCCTGGGTTCAAGCGATTCTCCTACATCAGCCTCCGA  
 GTAGCTGGGATTACAGGCATGCGCCACCAAGCCCCGCTAATTTTGTATTTTTTAGTAGAGACAGGGTTTCGC  
 CATGTTGGTCAGGCTTGTCTCGAACTCCTGGCCTCAGGTGATCCGCCTGTCTCGGCCTCCAGAATGCTGG  
 GATTATAGACGTGAGCCACCGCATCCGGACTTTCTTTTATGTAATAGTGATAATTCTATCCAAAGCATTTTTT  
 TTTTTTTTGGAGTGGAGTCTCATTCTGTCAACCCAGGCTGGAGGGTGGTGGCGCGATCTCGGCTTACTGCAA  
 CCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGAATTACACACGTGCGCCA  
 CCATGGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTGTCAACCATTTTGGCCAAGCTGGCCTCGAACTC  
 CTGACCTCAGGTGATCTGCCCCGCTCGGCTTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGTCTCT  
 GCTCCAAAGCATTTTTCTTTCTATGCCTCAAAACAAGATTGCAAGCCAGTCTCAAAGCGGATAATTCAAGAGC  
 TAACAGGTATTAGCTTAGGATGTGTGGCACTGTTCTTAAGGCTTATATGTATTAATACATCATTTAAACTCACA  
 ACAACCCCTATAAAGCAGGGGGCACTCATATCCCTTCCCCCTTTATAATTACGAAAAATGCAAGGTATTTTC  
 AGTAGGAAAGAGAAATGTGAGAAGTGTGAAGGAGACAGGACAGTATTGAAGCTGGTCTTTGGATCACTGTG  
 CAACTCTGCTTCTAGAACACTGAGCACTTTTTCTGGTCTAGGAATTATGACTTTGAGAATGGAGTCCGTCCTT  
 CCAATGACTCCCTCCCCATTTTCTATCTGCCTACAGGCAGAAATTCTCCCCGTCCGTATTAAATAAACCTCA  
 TCTTTTCAGAGTCTGCTCTTATACCAGGCAATGTACAGTCTGAGAAACCCTTGCCCCAGACAGCGCTTTTAC  
 ACGCAGGAGGGGAAGGGGAGGGGAAGGAGAGAGCAGTCCGACTCTCCAAAAGGAATCCTTTGAACTAGGG  
 TTTCTGACTTAGTGAACCCCGCGCTCCTGAAAATCAAGGGTTGAGGGGGTAGGGGGACACTTTCTAGTCGTA  
 CAGGTGATTTGATTCTCGGTGGGGCTCTCACAACCTAGGAAAGAATAGTTTTGCTTTTTCTTATGATTAAGA  
 AGAAGCCATACTTTCCCTATGACACCAAACACCCCGATTCAATTTGGCAGTTAGGAAGGTTGTATCGCGGAG  
 GAAGGAAACGGGGCGGGGGCGGATTCTTTTTAACAGAGTGAACGCACTCAAACACGCCTTTGCTGGCAGG  
 CGGGGAGCGCGGCTGGGAGCAGGAGCGGAGGGCGGTGCTGGGGGGCAGGTGGGGAGGAGCCAGT  
 CCTCCTTCTTGCCAACGCTGGCTCTGGCGAGGGCTGCTTCCGGCTGGTGCCCCCGGGGAGACCCAACC  
 TGGGGCGACTTCAGGGGTGCCACATTCTGCTAAGTCTCGGAGTTAATAGCACCTCCTCCGAGCACTCGCTC  
 ACGGCGTCCCCTTGCTGGAAGATACCGCGGTCCCTCCAGAGGATTTGAGGGACAGGGTGGGAGGGGGC  
 TCTTCCGCCAGCACCGGAGGAAGAAAGAGGAGGGGCTGGCTGGTCAACAGAGGGTGGGGCGGACCGCGT  
 GCGCTCGGCGGCTGCGGAGAGGGGGAGAGCAGGCAGCGGGCGGGGAGCAGCATGGAGCCGGCGGC  
 GGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGGCCGGGGTGGGTAGAGGAGGT  
 GCGGGCGCTGCTGGAGGCGGGGGCGCTGCCAACGCACCGAATAGTTACGGTGGGAGGCGGATCCAGGT  
 GGGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGGAATT  
 GGAATCAGGTAGCGCTTCGATTCTCCGAAAAAGGGGAGGCTTCTGGGGAGTTTTGAGAAGGGGTTTGT  
 ATCAGAGACCTCCTCCTGGCGACGCCCTGGGGCTTGGGAAGCCAAGGAAGAGGAATGAGGAGCCACGCG  
 CGTACAGATCTCTCGAATGCTGAGAAGATCTGAAGGGGGGAACATATTTGTATTAGATGGAAGTATGCTCTTT  
 ATCAGATACAAAATTTACGAACGTTTGGGATAAAAAGGGAGTCTTAAAGAAATGTAAGATGTGCTGGGACTAC  
 TTAGCCTCCAATTCACAGATACCTGGATGGAGCTTATCTTTCTTACTAGGAGGGATTATCAGTGGAAATCTGT  
 GGTGTATGTTGGAATAAATATCGAATATAAATTTTGTATCGAAATTATTCAGAAGCGGCCGGGGCGCGGTGCCTC  
 ACGCCTTGTAATCCCTTCACTTTGGGAGATCAAGGCGGGGGGAATCACCTGAGGTGGGAGTTTCGAGACCA  
 GCCTGGCCAACAGGTGAAACCTCGCCTCTACTAAAAATACAAAAAGTAGCCGGGGGTGGTGGCAGGCGCCT  
 GTAATCCCAGCTACTCGGGAGGTTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCTGAGGTTGTAGTGAAC  
 AGCAGATGGAGCTTCACTCCAGCCTGGGTGACAGAGTGAGACTTTGTGCAAGAAAGAAAGAGAGAA  
 AGAGAGAGAGAAAAATTATTCAGAAGCAACTACATATTGTGTTTATTTTTAACTGAGTAGGGCAAATAAATA  
 TGTTTGCTGTAGGAACCTAGGAAATAATGAGCCACATTGTGATCATTCCAGAGGTAATATGTAGTTACCAT  
 TTTGGGAATATCTGCTAACATTTTTGCTCTTTTACTATCTTTAGCTTACTTGATATAGTTTGTGATAAGAG  
 TTTTCAATTCCTCATTTTTGAACAGAGGTGTTTCTCCTCTCCCTACTCCTGTTTTGTGAGGGAGTTAGGGAG  
 GATTTAAAAGTAATTAATACATGGGTAACCTTAGCATCTCTAAATTTTGCCAACAGCTTGAACCCGGGAGTTTG  
 GCTTTGTAGTCTACAATATCTTAGAAGAGACCTTATTTGTTAAAAACAAAAAGGAAAAAGAAAGTGGATAG  
 TTTTGACAATTTTTAATGGAG

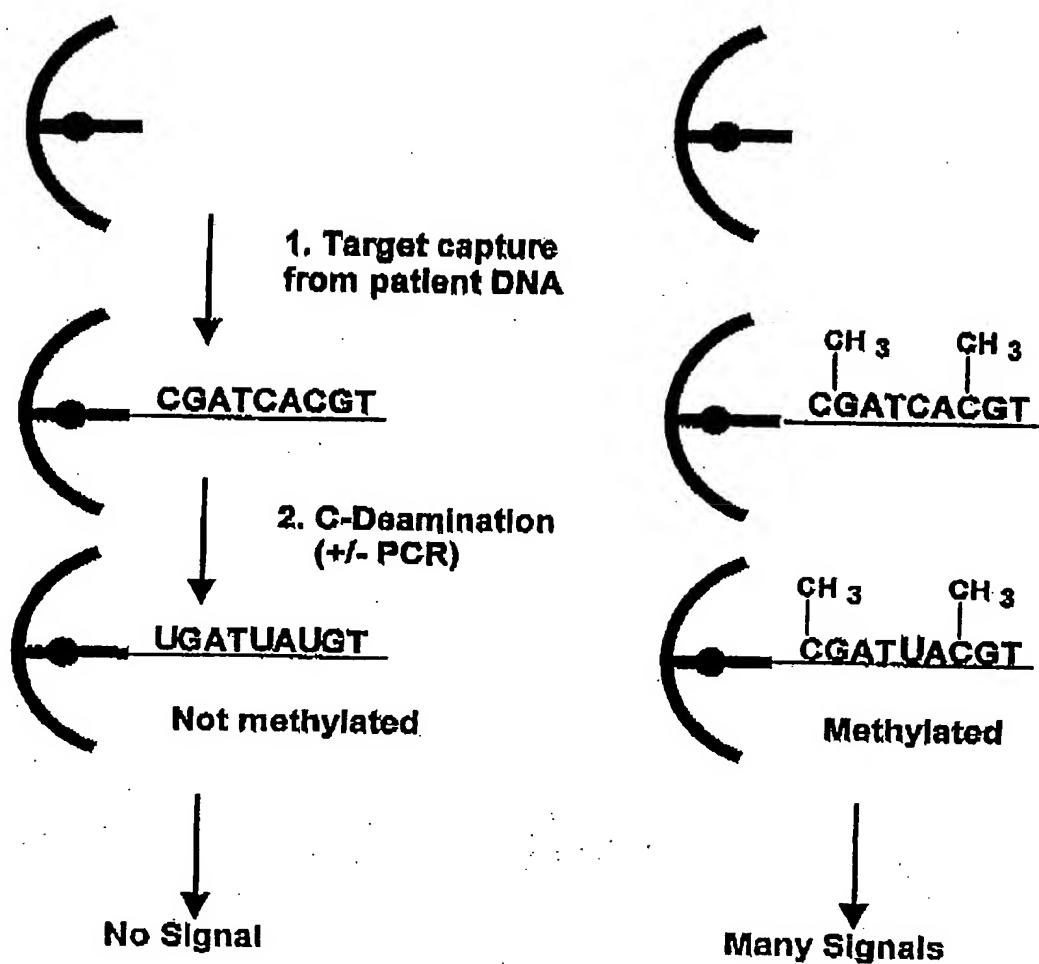


FIGURE 31

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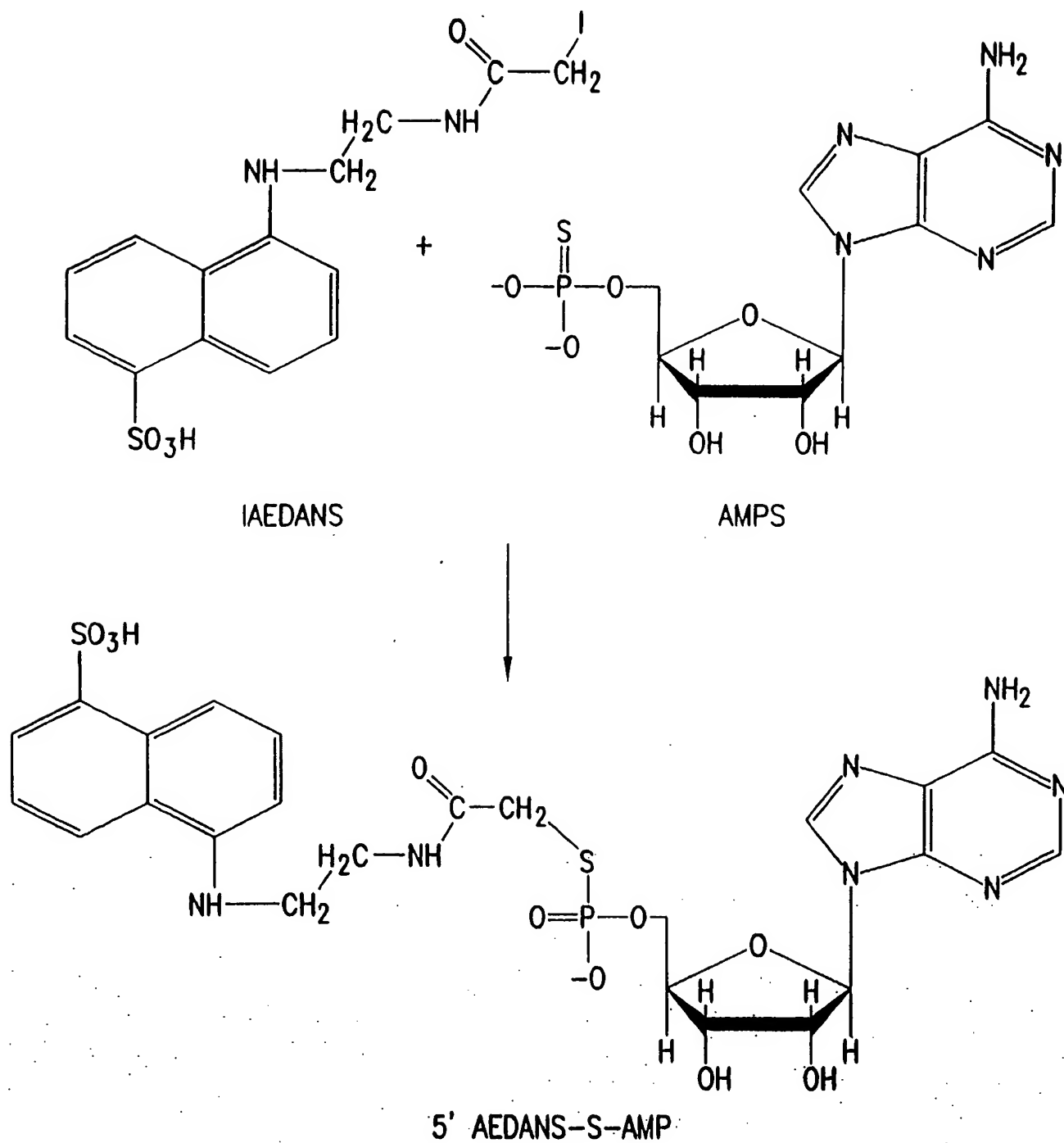


FIG.3



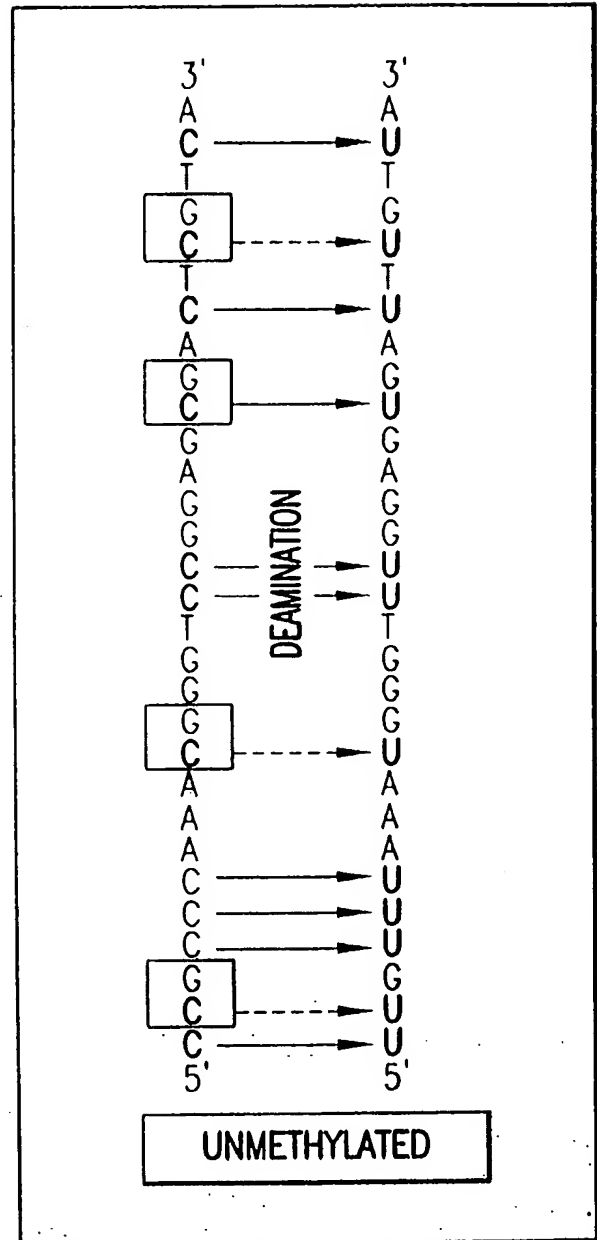
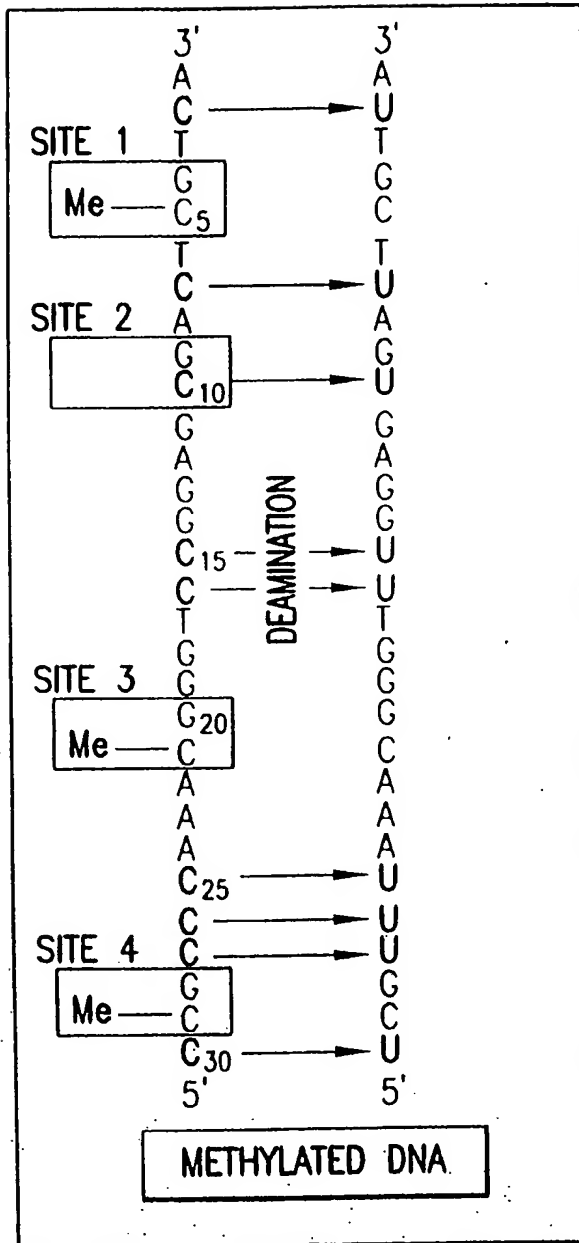
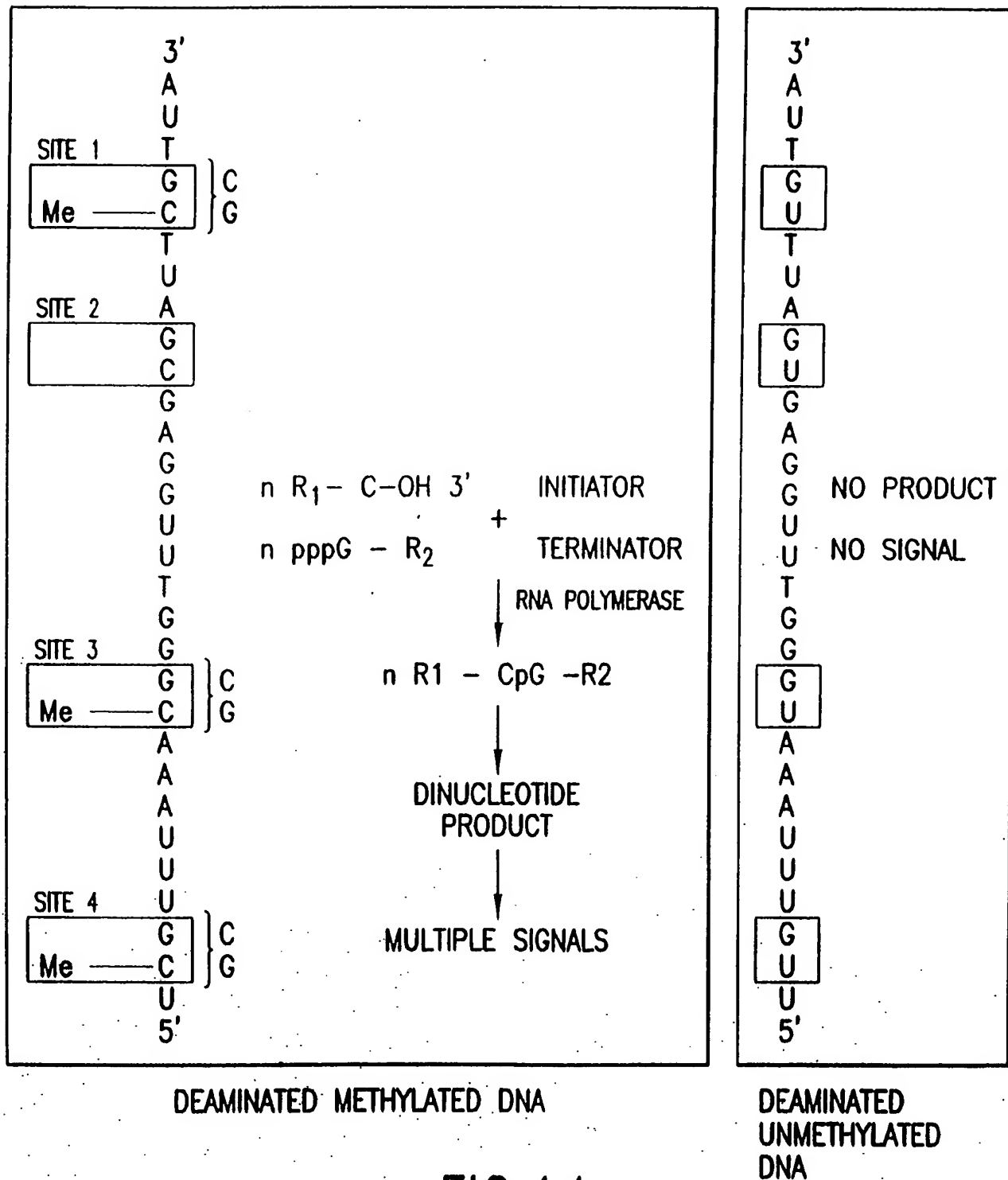
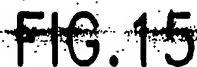


FIG.13



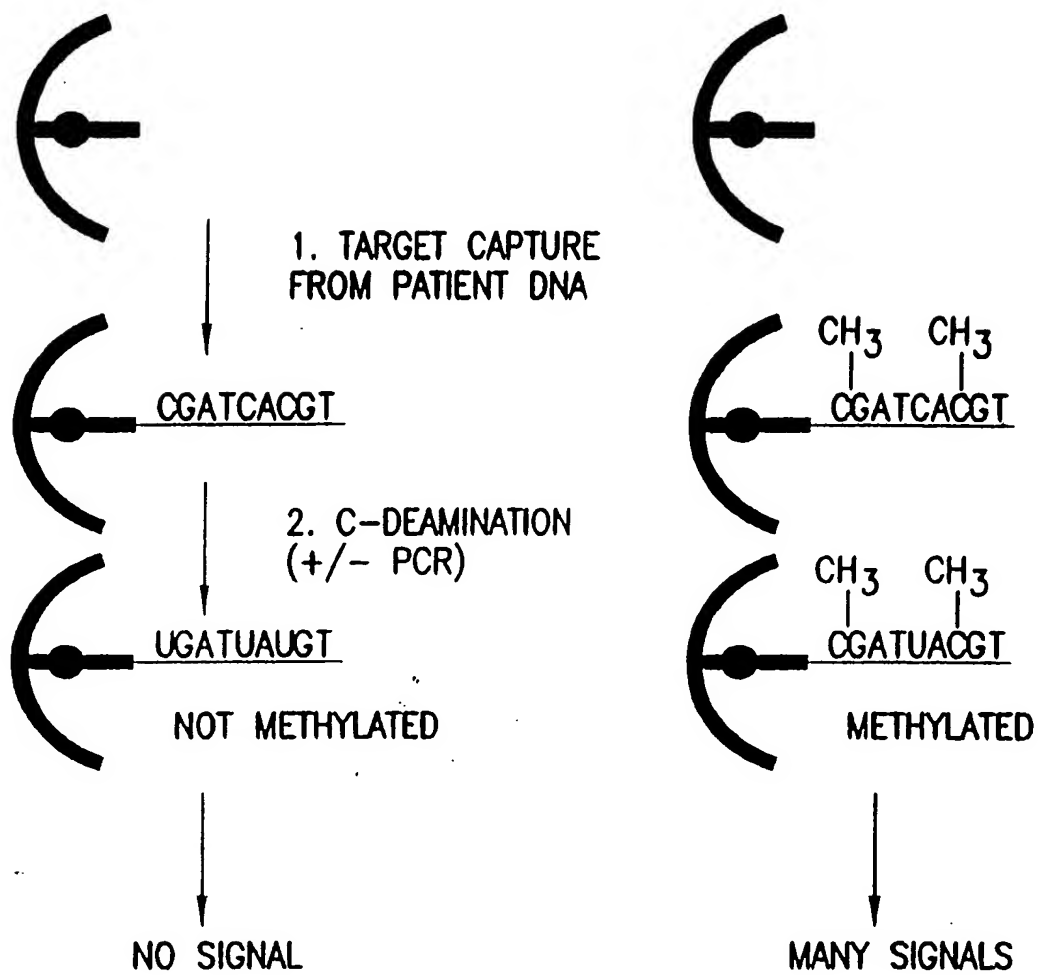


ATATAC TGGGTC TACAAGGTTTAAAGTCAACCAGGGATTGAAATATAACTTTTAAACAGAGCTGGATTATCCAGT  
AGGCAGATTAAGCATGTGCTTAAGGCATCAGCAAAGTCTGAGCAATCCATTTTTTAAAACGTAGTACATGTTTT  
TGATAAGCTTAAAAAGTAGTAGTCACAGGAAAAATTAGAACTTTTACCTCCTTGCGCTTGTTATACTCTTTAGT  
GCTGTTTAACTTTTTCTTTGTAAGTGAGGGTGGTGGAGGGTGCCATAATCTTTTCAGGGAGTAAGTTCTTCTT  
GGTCTTTCTTTCTTTCTTTCTTTCTTTTTCTTGAGACCAAGTTTCGCTCTTGCTCCCAGGCTGGAGTGCAA  
TGGCGGATCTCGGCTCACTGCAACCTCCGCTTCTCCTGGGTTCAAGCGATTCTCCTACATCAGCCTCCGA  
GTAGCTGGGATTACAGGCATGCGCCACCAAGCCCCGCTAATTTTGTATTTTTTAGTAGAGACAGGGTTTCGC  
CATGTTGGTCAGGCTTGCTCTCGAACTCCTGGCCTCAGGTGATCCGCCTGTCTCGGCCTCCAGAATGCTGG  
GATTATAGACGTGAGCCACCGCATCCGACTTTCTTTTATGTAATAGTGATAATTCTATCCAAAGCATTTTTT  
TTTTTTTTTGAGTCGGAGTCTCATTCTGTCACCCAGGCTGGAGGGTGGTGGCGGATCTCGGCTTACTGCAA  
CCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGAATTACACACGTGCGCCA  
CCATGGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGTGTCAACATTTTGGCCAAGCTGGCCTCGAACTC  
CTGACCTCAGGTGATCTGCCCGCTCGGCTTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGTCCT  
GCTCCAAAGCATTTTCTTTCTATGCCTCAAAACAAGATTGCAAGCCAGTCTCAAAGCGGATAATTCAAGAGC  
TAACAGGTATTAGCTTAGGATGTGTGGCACTGTTCTTAAGGCTTATATGTATTAATACATCATTTAAACTCACA  
ACAACCCCTATAAAGCAGGGGGCACTCATATTCCTTCCCCCTTTATAATTACGAAAAATGCAAGGTATTTTC  
AGTAGGAAAGAGAAATGTGAGAAGTGTGAAGGAGACAGGACAGTATTTGAAGCTGGTCTTTGGATCACTGTG  
CAACTCTGCTTCTAGAACACTGAGCACTTTTCTGGTCTAGGAATTATGACTTTGAGAATGGAGTCCGTCCCTT  
CCAATGACTCCCTCCCCATTTTCTATCTGCCTACAGGCAGAATTCTCCCCCGTCCGTATTAAATAAACCTCA  
TCTTTTCAGAGTCTGCTCTTATACCAGGCAATGTACAGCTCTGAGAAACCTTGCCCCAGACAGCCGTTTTAC  
ACGCAGGAGGGGAAGGGGAGGGGAAGGAGAGAGCAGTCCGACTCTCCAAAAGGAATCCTTTGAACTAGGG  
TTTCTGACTTAGTGAACCCCGCGCTCCTGAAAATCAAGGGTTGAGGGGGTAGGGGGACACTTTCTAGTCGTA  
CAGGTGATTTGATTCTCGGTGGGGCTCTCACAAGTGAAGAAAGATAGTTTTGCTTTTTCTTATGATTAAGA  
AGAAGCCATACTTTCCCTATGACACCAAACACCCCGATTCAATTTGGCAGTTAGGAAGGTTGTATCGCGGAG  
GAAGGAAACGGGGCGGGGGCGGATTTCTTTTAAACAGAGTGAACGCACTCAAACACGCCTTTGCTGGCAGG  
CGGGGGAGCGCGCTGGGAGCAGGGAGGCCGGAGGGCGGTGTGGGGGCAGGTGGGAGGAGCCAGT  
CCTCCTTCTTGCCAACGCTGGCTCTGGCGAGGGCTGCTTCCGGCTGGTGCCCCGGGGGAGACCCAACC  
TGGGGCGACTTCAGGGGTGCCACATTCGCTAAGTGCTCGGAGTTAATAGCACCTCCTCCGAGCACTCGCTC  
ACGGCGTCCCCTTGCTGGAAAGATACCGCGGTCCCTCCAGAGGATTTGAGGGACAGGGTCCGAGGGGGC  
TCTTCCGCCAGCACCGGAGGAAGAAAGAGGAGGGCTGGCTGGTCACCAGAGGGTGGGGCGGACCGCGT  
GCGCTCGGCGGCTGCGGAGAGGGGGAGAGCAGGCAGCGGGCGGCGGGGAGCAGCATGGAGCCGGCGGC  
GGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTGGGTAGAGGAGGT  
GCGGGCGCTGCTGGAGGCGGGGGCGCTGCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGT  
GGGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGGAATT  
GGAATCAGGTAGCGCTTCGATTCTCCGAAAAAGGGAGGCTTCTGGGGAGTTTTCAGAAGGGGTTTGT  
ATCACAGACCTCCTCCTGGCGACGCCCTGGGGCTTGGGAAGCCAAGGAAGAGGAATGAGGAGCCACGCG  
CGTACAGATCTCTCGAATGCTGAGAAGATCTGAAGGGGGGAACATATTTGTATTAGATGGAAGTATGCTCTTT  
ATCAGATACAAAATTTACGAACGTTTGGGATAAAAAAGGGAGTCTTAAAGAAATGTAAGATGTGCTGGGACTAC  
TTAGCCTCCAATTCACAGATACCTGGATGGAGCTTATCTTTCTTACTAGGAGGGATTATCAGTGGAATCTGT

FIG. 29A

GGTGTATGTTGGAATAAATATCGAATATAAATTTTGATCGAAATTATTCAGAAGCGGCCGGGCGCGGTGCCTC  
ACGCCTTGTAATCCCTTCACTTTGGGAGATCAAGGCGGGGGGAATCACCTGAGGTCGGGAGTTCGAGACCA  
GCCTGGCCAACAGGTGAAACCTCGCCTCTACTAAAAATACAAAAAGTAGCCGGGGGTGGTGGCAGGCGCCT  
GTAATCCCAGCTACTCGGGAGGTTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCTGAGGTTGTAGTGAAC  
AGCGAGATGGAGCCACTTCACTCCAGCCTGGGTGACAGAGTGAGACTTTGTGAAAGAAAGAAAGAGAGAA  
AGAGAGAGAGAAAAATTATTCAGAAGCAACTACATATTGTGTTTATTTTAACTGAGTAGGGCAAATAAATATA  
TGTTTGCTGTAGGAACCTAGGAAATAATGAGCCACATTCATGTGATCATTCCAGAGGTAATATGTAGTTACCAT  
TTTGGGAATATCTGCTAACATTTTGTCTTTTACTATCTTTAGCTTACTTGATATAGTTTATTTGTGATAAGAG  
TTTTCAATTCCTCATTTTTGAACAGAGGTGTTTCTCCTCTCCCTACTCCTGTTTTGTGAGGGAGTTAGGGGAG  
GATTTAAAAGTAATTAATACATGGGTAAGTATGATCTCTAAAATTTTGCCAACAGCTTGAACCCGGGAGTTTG  
GCTTTGTAGTCCTACAATATCTTAGAAGAGACCTTATTTGTTTAAAAACAAAAAGGAAAAAGAAAAGTGGATAG  
TTTTGACAATTTTAAATGGAG

**FIG. 29B**



**FIG. 30**